**Application No.:** 

10/589,233

Filing Date:

**January 16, 2007** 

## AMENDMENTS TO THE CLAIMS

1. (Currently amended) A recombinant nucleotide sequence which codes upon expression a bifunctional hybrid active-site serine  $\beta$ -lactamase protein, wherein the  $\beta$ -lactamase protein is a class A, C or D  $\beta$ -lactamase protein that bears at least one heterologous sequence, wherein the  $\beta$ -lactamase protein bears the at least one heterologous sequence in a region forming a juncture between alpha-helix 8 and alpha helix 9 of said active-site serine  $\beta$ -lactamase in a region located between two neighboring alpha helices of the  $\beta$ -lactamase sequence, wherein the region is selected from the group consisting of:

- a) a region forming a juncture between alpha helix 8 and alpha helix 9 of TEM-1
   β-lactamase; and
- b) a region forming a juncture between the alpha helices of said class A, C or D
  β-lactamase, said alpha helices corresponding to the alpha helix 8 and alpha
  helix 9 of the TEM-1 β-lactamase, and

wherein the hybrid protein <u>has</u> two functions, wherein, in said bifunctional hybrid protein, the first function is associated with the  $\beta$ -lactamase portion and the second function is associated with the at least one heterologous sequence having a biological function which is different from the first function.

## 2.-5. (**Canceled**)

- 6. (Previously presented) The recombinant nucleotide sequence according to Claim 1, wherein the  $\beta$ -lactamase moiety is a class A  $\beta$ -lactamase, wherein said  $\beta$ -lactamase class A protein bears the at least one heterologous sequence in the region forming a juncture between alpha helix 8 and alpha helix 9.
- 7. **(Previously presented)** The recombinant nucleotide sequence according to claim 1, wherein the region forming a juncture between alpha helix 8 and alpha helix 9 is selected from the group consisting of:
  - a) amino acid sequence Thr195 to Leu199 of the TEM-1 β-lactamase; and
  - b) an amino acid sequence in a  $\beta$ -lactamase other than TEM-1  $\beta$ -lactamase corresponding to the amino acid sequence Thr195 to Leu199 in TEM-1  $\beta$ -lactamase.

## 8.-11. (Canceled)

**Application No.:** 

10/589,233

Filing Date:

January 16, 2007

12. (Currently amended) A recombinant nucleotide sequence which codes upon expression a bifunctional hybrid class A  $\beta$ -lactamase elass A protein, wherein the class A  $\beta$ -lactamase elass A protein bears at least one heterologous sequence in a region located between two neighboring alpha helices of the  $\beta$ -lactamase sequence, wherein the region is selected from the group consisting of:

- a) the <u>a</u> region forming a juncture between alpha helix 8 and alpha helix 9 of the TEM-1 β-lactamase; and
- b) the <u>a</u> region forming a juncture between the alpha helices of <u>said a homologous</u> <u>class A  $\beta$ -lactamase class A</u>, said alpha helices corresponding to the alpha helix 8 and alpha helix 9 of the TEM-1  $\beta$ -lactamase,

wherein the hybrid protein has a first function and a second function, wherein the first function is associated with the  $\beta$ -lactamase portion and is selected from the group consisting of:

- c) hydrolyzing  $\beta$ -lactams ( $\beta$ -lactamase activity); and
- d) binding covalently and in a stable manner to substances selected from the group consisting of  $\beta$ -lactams, derivatives of  $\beta$ -lactams, and inhibitors of  $\beta$ -lactams; and wherein the second function is associated with the at least one heterologous sequence having a biological function which is different from the first function.

## 13.-15. (Canceled)

- 16. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence has a length of 11 or more amino acid residues.
- 17. **(Previously presented)** The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence has a length of 18 or more amino acid residues.
- 18. (Previously presented) The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence has a length of 25 or more amino acid residues.
- 19. (Previously presented) The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence has a length of 50 or more amino acid residues.
- 20. (Previously presented) The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence has a length of 100 or more amino acid residues.

**Application No.:** 10/589,233

Filing Date: January 16, 2007

21. (Currently amended) The recombinant nucleotide sequence according to Claim 1, wherein the nucleotide sequence coding for the β-lactamase sequence encodes is selected from the group consisting of:

- a) nucleotide sequence coding for the β-lactamase TEM-1 (SEQ-ID-NO: 1)
- b) nucleotide sequence coding for the β-lactamase BlaP (SEQ I D NO: 2);
- e) nucleotide sequence coding for the β-lactamase BlaL (SEQ ID NO: 3);
- d) nucleotide sequence coding for the β-lactamase AmpC (SEQ ID NO: 39); and
- e) nucleotide sequence coding for the β-lactamase BlaR-CTD (SEQ-ID-NO: 41);
- f) a recombinant sequence of one or more of a) to e); and
- g) nucleotide sequences which hybridize under stringent conditions to the nucleotide sequences of any one of a) to f).
- 22. (Currently amended) The recombinant nucleotide sequence according to Claim 1, wherein the at least one heterologous sequence is related to a function selected from the group consisting of: being an epitope, being a specific binding partner for antibodies, being a sequence that is specifically recognized and bound by antibodies, a sequence having a binding affinity to earth alkali and metal ions, a sequence having enzymatic activity, being a toxin, (STa heat-stable enterotoxin of *E. coli*), bearing a glycosylation site, bearing a glycosylated peptide, being a specific binding partner for any polypeptide or any ligand, and a sequence having a binding affinity to dsDNA, and ssDNA or RNA—(having—a binding affinity—to—nucleotide—and polynucleotide).
- 23. (Currently amended) The recombinant nucleotide sequence according to Claim 1, wherein the at least one <u>nucleic acid sequence encoding the at least one</u> heterologous sequence is selected from the group consisting of: STa (heat stable enterotoxin of *Escherichia coli*, SEQ ID NO: 21), encodes protein A of *Staphylococcus aureus* with two Fc Binding domains, (SEQ ID NO: 23 and 25), protein G of *Streptococcus pyogenes*, (SEQ ID NO: 27 and 29), a linear antigenic determinant of the hemagglutinin of the Influenza virus (SEQ ID NO: 31), a fragment of human phospholipase-type 11 (hPLA2) (SEQ ID NO: 33), and LPS binding amino acid sequence (SEQ ID NO: 35), and nucleotide sequences which hybridize under stringent conditions to said nucleotide sequences.

24.-53. (Canceled)